

D. Hartman

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



PH# 1

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/147,801A  
Art Unit / Team No. : 1645  
Date Processed by STIC: 5/11/2000

RECEIVED  
MAY 23 2000  
TC 1600 MAIL ROOM

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/147,801A

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      **(2) INFORMATION FOR SEQ ID NO:X:**  
                                 **(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 **(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
                                 **This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      **<210> sequence id number**  
                                 **<400> sequence id number**  
                                 **000**
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS  
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE  
DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

1645

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/147,801A

DATE: 05/11/2000  
TIME: 16:08:10

Input Set : A:\PICORNAL.txt  
Output Set: N:\CRF3\05112000\I147801A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: NIKLASSON, Bo  
5 <120> TITLE OF INVENTION: NEW PICORNA VIRUSES, VACCINES AND DIAGNOSTIC KITS  
7 <130> FILE REFERENCE: REF/Niklasson/801  
9 <140> CURRENT APPLICATION NUMBER: 09/147,801A  
C--> 10 <141> CURRENT FILING DATE: 1999-03-11  
12 <150> PRIOR APPLICATION NUMBER: PCT/SE97/01515  
13 <151> PRIOR FILING DATE: 1997-09-09  
15 <160> NUMBER OF SEQ ID NOS: 4  
17 <170> SOFTWARE: PatentIn Ver. 2.1  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 264  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Picornaviridae  
24 <400> SEQUENCE: 1  
25 agtctagtct tctcttgat gtgtcctgca ctgaacttgt ttctgtctct ggagtgtctt 60  
26 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacagggtg 120  
27 ctttcacctc tggacagtgc attccacacc cgctccacgg tagaagatga tgtgtgtctt 180  
28 tgcttggtaa aagcttgta aaatcgtgtg taggcgtagc ggctacttga gtgccagcgg 240  
29 attacccta gtgtaaacac tagc 264  
32 <210> SEQ ID NO: 2  
33 <211> LENGTH: 264  
34 <212> TYPE: DNA  
35 <213> ORGANISM: Picornaviridae  
37 <400> SEQUENCE: 2  
38 agtctagttt cattctgtgt gtgtttggca ctgaaattat ttctgtctct ggggtgtctt 60  
W--> 39 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacagggtg 120  
40 ctttcacctc tggacagtgc attccacacc cgctccacag tagaagatga tgtgtgtctt 180  
W--> 41 tgcttggtaa aagcttgta aaatcgtgtg taggcgtagc ggctacttga gtgccagcgg 240  
W--> 42 attacccta gtgtaaacac tagc 264  
45 <210> SEQ ID NO: 3  
46 <211> LENGTH: 264  
47 <212> TYPE: DNA  
48 <213> ORGANISM: Picornaviridae  
50 <400> SEQUENCE: 3  
51 agtttggttc tctcttgagt gtgttttggt ttagcataat ttctgtctct agagtgtctt 60  
52 acactctagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacagggtg 120  
53 ctttcacctc tggacagtgc attccatacc cgctccacaa tagaagatga tgtatatctt 180  
54 tgtttggtaa atgctcatga aacgtgtgtg taggcgtagc ggctacttga atgccagcgg 240  
55 aaccccccta gtgtaaacac tagc 264  
58 <210> SEQ ID NO: 4  
59 <211> LENGTH: 179  
60 <212> TYPE: PRT  
61 <213> ORGANISM: Picornaviridae  
63 <400> SEQUENCE: 4  
64 Lys Asp Leu Met Glu Ile Ala Arg Met Pro Ser Val Tyr Lys Gly Glu  
65 1 5 10 15  
67 Arg Thr Glu Pro Gly Gly Thr Asn Gly Tyr Phe Gln Trp Ser His Thr

see item 10 on Enn Summary Sheet

## RAW SEQUENCE LISTING

DATE: 05/11/2000

PATENT APPLICATION: US/09/147,801A

TIME: 16:08:10

Input Set : A:\PICORNAL.txt

Output Set: N:\CRF3\05112000\I147801A.raw

```

68          20          25          30
70 His Ser Pro Ile Asn Trp Val Phe Asp Gly Gly Ile His Leu Glu Asp
71          35          40          45
73 Met Pro Asn Leu Asn Leu Phe Ser Ser Cys Tyr Asn Tyr Trp Arg Gly
74          50          55          60
76 Ser Thr Val Leu Lys Leu Thr Val Tyr Ala Ser Thr Phe Asn Lys Gly
77 65          70          75          80
79 Arg Leu Arg Met Ala Phe Phe Pro Ile Met Met Gln Gly Thr Gln Arg
80          85          90          95
82 Lys Lys His Lys Cys Leu Phe Met Val Cys Asp Ile Gly Leu Asn Asn
83          100          105          110
85 Thr Phe Glu Met Thr Ile Pro Tyr Thr Trp Gly Asn Trp Met Arg Pro
86          115          120          125
88 Thr Arg Gly Ser Val Ile Gly Trp Leu Arg Ile Asp Val Leu Asn Arg
89          130          135          140
91 Leu Thr Tyr Asn Ser Ser Ser Pro Asn Ala Val Asn Cys Ile Leu Gln
92 145          150          155          160
94 Val Lys Met Gly Asn Asp Ala Lys Phe Met Val Pro Thr Thr Ser Asn
95          165          170          175
97 Ile Val Trp

```

## VERIFICATION SUMMARY

DATE: 05/11/2000

PATENT APPLICATION: US/09/147,801A

TIME: 16:08:11

Input Set : A:\PICORNAL.txt

Output Set: N:\CRF3\05112000\I147801A.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:39 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:39 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2  
L:39 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2  
L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:39 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
L:41 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:41 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2  
L:41 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2  
L:41 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
M:340 Repeated in SeqNo=2  
L:42 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:42 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2  
L:42 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2  
L:42 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2